

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/524,860
Source: pg 110
Date Processed by STIC: 3/2/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/524,860
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



PCT

RAW SEQUENCE LISTING

DATE: 03/02/2005

PATENT APPLICATION: US/10/524,860

TIME: 13:07:31

Input Set : A:\PH-1839PCT-US(sequence).txt

Output Set: N:\CRF4\03022005\J524860.raw

3 <110> APPLICANT: Nichirei Corporation
 5 <120> TITLE OF INVENTION: Method of the detection of Vibrio vulnificus and primers
 and probes
 6 therefor
 8 <130> FILE REFERENCE: PH-1839-PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/524,860
 C--> 10 <141> CURRENT FILING DATE: 2005-02-18
 10 <150> PRIOR APPLICATION NUMBER: JP 2002-255126
 11 <151> PRIOR FILING DATE: 2002-08-30
 13 <160> NUMBER OF SEQ ID NOS: 20
 15 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 819
 42 <212> TYPE: DNA
 W--> 43 <213> ORGANISM:
 45 <400> SEQUENCE: 2
 46 actcgtgaag gcgaaatcga catcgctaam cgaattgaag atggtatcaa ccaagtacag 60
 47 tcstctgttg ctgaataccc aggaaccatt ccttatattc tkgaacagtt cgacaaagta 120
 48 caagcggaag aacttcgcct mactgatctt atcagtggtt ttggtgatcc aaatgcagat 180
 49 gaaacggcwg ctccaaccgc aacacacaty ggttcagagc ttgcagaatc tgatttggaa 240
 E--> 50 gatgaagaca ayaccgacat cgacgatgaa gacgaagaynnnnnngaaga tggcgattca 300
 51 agcagygtt cagaggamga tgcggcatc gaccctgaaa tggcgctaga gaagttyact 360
 52 caretctgta acagctayca gaacttgcaa cttgcktra atgaacatgg tcgagagagt 420
 53 gctcaaacag ctcaagccca tgaactgatg ctgatgtgt ttaaagagtt tgcgtctaacd 480
 54 ccgaagcagt ttgaccattt ggtaacgaa cttcgcaccg cyatggatcg cggtcgtagc 540
 55 caagarcgyt tgatcatgaa rtctgcggta gaaatcgcsa aratgccraa gaartcktty 600
 56 atygcwctct tyactggcaa cgartcwaro gaagaatggt tagatmagat cctmgyytct 660
 57 gayaagccrt acgyagaaaa gatyaarctk cacgaagaag acattcgtcg ttcaatcdcc 720
 58 aagctaagag caattgaaga agaaacgtcg ctttcagtra rcaacatcaa agacatcagc 780
 59 cgtcgtatgt ctatmggtga agcmaaagct cgccgtgcg 819
 62 <210> SEQ ID NO: 3
 63 <211> LENGTH: 648
 64 <212> TYPE: DNA
 W--> 65 <213> ORGANISM:
 67 <400> SEQUENCE: 3
 68 ccaatgggccc gtatcgttga aatttttggg ccagaatctt caggtaaaac cacgttgacc 60
 69 cttgagctga tcgctgcrge tcaacgtgaa ggcaaaactt gtgcgtttat cgatgcygag 120
 70 cacgcgttrg atcctgtgta tgcgaagaar cttggcgatwa atatcgacca rtrrttggtg 180
 71 tctcagccyg ayacbggtga acaagcrttg gaaatctgtg atgckettgc tcgctcaggk 240
 72 gcggttgayg ttattgttgt cgaytctgk gcmgcattga crccaaaggc agaaatyga 300

pp 1-3
 Does Not Comply
 Corrected Diskette Needed

(same error in sequence 1)

mandatory response needed - see item 10 on Error

summary sheet

see p. 3 for error explanation

mandatory response needed
 see p. 2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/524,860

DATE: 03/02/2005

TIME: 13:07:31

Input Set : A:\PH-1839PCT-US(sequence).txt

Output Set: N:\CRF4\03022005\J524860.raw

E--> 73 ggtgagatgg ggyaytcgca catgggtctn caagctcgta tgctmtctca agcgatgcgt 360
74 aagytaacgg gkaacctaaa rcagtctaac tgtatgtgta tcttcatyaa ccagatycgt 420
75 atgaagatyg gkgtgatggt tggtaaycca gaaaccacaa crggtggtaa cgcwctgaaa 480
76 ttctacgctt ctgtwcgtct tgatattcgc cgtactggtg cratcaaaga aggygatgag 540
77 gtmgtgggta aygaaacgcg yatcaaagtg gtgaagaata agatcgctgc gccgttttaa 600
78 gaagccaaya cycaaattat gtayggccar ggcwtttaacc gygaaggy 648
269 <210> SEQ ID NO: 20
270 <211> LENGTH: 21
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
277 <400> SEQUENCE: 20
278 tcaaccgcmc ctgagcgagc a 21
E--> 280 1/10

*delete**see p. 3
for error
explanation*

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/524,860

DATE: 03/02/2005

TIME: 13:07:32

Input Set : A:\PH-1839PCT-US(sequence).txt

Output Set: N:\CRF4\03022005\J524860.raw

error explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:2; N Pos. 280,281,282,283,284,285

Seq#:3; N Pos. 330

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/524,860

DATE: 03/02/2005

TIME: 13:07:32

Input Set : A:\PH-1839PCT-US(sequence).txt

Output Set: N:\CRF4\03022005\J524860.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:201 W: Mandatory field data missing, <213> ORGANISM
L:43 M:201 W: Mandatory field data missing, <213> ORGANISM
L:50 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:65 M:201 W: Mandatory field data missing, <213> ORGANISM
L:73 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:167 M:283 W: Missing Blank Line separator, <220> field identifier
L:253 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:254 E: No. of Bases conflict, LENGTH:Input:10 Counted:22 SEQ:20
L:280 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:22 SEQ:20